

JOURNAL J. Biol. Chem. 267 (34), 24575-24584 (1992)
 PUBMED 1339443
 REMARK NUCLEOTIDE SEQUENCE [GENOMIC DNA].
 Erratum: [J Biol Chem 1993 Aug 25;268(24):18398]
 3 (residues 1 to 359)
 REFERENCE Cameron, H.S., Szczepaniak, D. and Weston, B.W.
 AUTHORS Expression of human chromosome 19p alpha(1,3)-fucosyltransferase
 TITLE genes in normal tissues. Alternative splicing, polyadenylation, and
 isoforms
 JOURNAL J. Biol. Chem. 270 (34), 20112-20122 (1995)
 PUBMED 7650030
 REMARK NUCLEOTIDE SEQUENCE [MRNA].
 TISSUE=Kidney
 COMMENT On or before Jul 18, 2007 this sequence version replaced
 gi:2134726, gi:2134727, gi:539596.
 [FUNCTION] Enzyme involved in the biosynthesis of the E-Selectin
 ligand, sialyl-Lewis X. Catalyzes the transfer of fucose from
 GDP-beta-fucose to alpha-2,3 sialylated substrates.
 [CATALYTIC ACTIVITY] GDP-beta-L-fucose +
 beta-D-galactosyl-(1->3)-N-acetyl-D-glucosaminyl-R = GDP +
 beta-D-galactosyl-(1->3)-(alpha-L-fucosyl-(1->4))-N-acetyl-beta-D-
 glucosaminyl-R.
 [PATHWAY] Protein modification; protein glycosylation.
 [SUBCELLULAR LOCATION] Golgi apparatus, Golgi stack membrane;
 Single-pass type II membrane protein. Note=Membrane-bound form in
 trans cisternae of Golgi.
 [ALTERNATIVE PRODUCTS] Event=Alternative splicing; Named
 isoforms=2; Name=1; IsoId=P51993-1; Sequence=Displayed; Name=2;
 IsoId=P51993-2; Sequence=VSP_001780.
 [TISSUE SPECIFICITY] Kidney, liver, colon, small intestine,
 bladder, uterus and salivary gland.
 [SIMILARITY] Belongs to the glycosyltransferase 10 family.
 [WEB RESOURCE] Name=GGDB; Note=GlycoGene database;
 URL=<http://ggdb.muse.aist.go.jp/GGDB/index.jsp>.
 FEATURES Location/Qualifiers
 source 1..359
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 gene 1..359
 /gene="FUT6"
 /note="synonym: FCT3A"
 Protein 1..359
 /gene="FUT6"
 /product="Alpha-(1,3)-fucosyltransferase"
 /EC_number="2.4.1.65"
 Region 1..359
 /gene="FUT6"
 /region_name="Mature chain"
 /experiment="experimental evidence, no additional details
 recorded"
 /note="Alpha-(1,3)-fucosyltransferase."
 /FTId=PRO_0000221110."
 Region 1..14
 /gene="FUT6"
 /region_name="Topological domain"
 /inference="non-experimental evidence, no additional
 details recorded"
 /note="Cytoplasmic (Potential)."
 Region 5..358
 /gene="FUT6"